

WHAT IS CLAIMED IS:

- 1 1. A hybrid polymerase having polymerase activity, wherein the
2 polymerase comprises SEQ ID NO:23 and is at least 80% identical over 700 contiguous
3 amino acids of the *Pyrococcus furiosus* (*Pfu*) polymerase sequence set forth in SEQ ID NO:
4 24 or at least 80% identical over 700 contiguous amino acids of the *Pyrococcus sp.* GB-D
5 polymerase sequence set forth in SEQ ID NO:25, with the *proviso* that
6 (a) when the polymerase is at least 85% identical to SEQ ID NO:24, the
7 sequence comprises at least one hybrid position that is mutated from the native *Pfu* residue to
8 the residue that occurs at the corresponding position of SEQ ID NO:25, wherein the hybrid
9 position is one of the residues designated as "X" in SEQ ID NO:26; or
10 (b) when the polymerase is at least 85% identical to SEQ ID NO:25, the
11 sequence comprises at least one hybrid position that is mutated from the native *Pyrococcus*
12 *sp.* GB-D residue to the residue that occurs at the corresponding position of SEQ ID NO:24,
13 wherein the hybrid position is one of the residues designated as "X" in SEQ ID NO:26.
- 1 2. The hybrid polymerase of claim 1, wherein the polymerase is at least
2 90% identical over 700 contiguous amino acids of the *Pfu* sequence set forth in SEQ ID
3 NO:24 or at least 90% identical over 700 contiguous amino acids of the *Pyrococcus sp.* GB-
4 D sequence set forth in SEQ ID NO:25.
- 1 3. The hybrid polymerase of claim 1, wherein the hybrid polymerase
2 comprises at least ten hybrid positions that are mutated from the native residue of SEQ ID
3 NO:24 or SEQ ID NO:25 to the corresponding residue of SEQ ID NO:25 or SEQ ID NO:24.
- 1 4. The hybrid polymerase of claim 1, wherein the hybrid polymerase
2 comprises at least twenty hybrid positions that are mutated from the native residue of SEQ ID
3 NO:24 or SEQ ID NO:25 to the corresponding residue of SEQ ID NO:25 or SEQ ID NO:24.
- 1 5. The hybrid polymerase of claim 1, wherein the hybrid polymerase
2 comprises at least forty hybrid positions that are mutated from the native residue of SEQ ID
3 NO:24 or SEQ ID NO:25 to the corresponding residue of SEQ ID NO:25 or SEQ ID NO:24.
- 1 6. The hybrid polymerase of claim 1, wherein the hybrid polymerase
2 comprises at least fifty hybrid positions that are mutated from the native residue of SEQ ID
3 NO:24 or SEQ ID NO:25 to the corresponding residue of SEQ ID NO:25 or SEQ ID NO:24.

- 1 7. The hybrid polymerase of claim 1, wherein the hybrid polymerase
2 comprises an amino acid sequence of SEQ ID NO:2, SEQ ID NO:12, SEQ ID NO:16, or
3 SEQ ID NO:18; or the polymerase region of SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8,
4 SEQ ID NO:10, SEQ ID NO:14, or SEQ ID NO:20.
- 1 8. The hybrid polymerase of claim 1, further comprising a DNA binding
2 domain.
- 1 9. The hybrid polymerase of claim 8, wherein the DNA binding domain
2 is selected from the group consisting of Sso7d, Sac7d, and Sac7e.
- 1 10. The hybrid polymerase of claim 9, wherein the DNA binding domain
2 is Sso7d.
- 1 11. The hybrid polymerase of claim 10 comprising an amino acid sequence
2 of SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8, SEQ ID NO:10, SEQ ID NO:14, or SEQ ID
3 NO:20.
- 1 12. An isolated nucleic acid enclosing a hybrid polymerase as set forth in
2 claim 1 or claim 8.
- 1 13. An expression vector comprising the nucleic acid of claim 12.
- 1 14. A host cell transfected with the vector of claim 13.
- 1 15. An isolated nucleic acid encoding a polypeptide comprising an amino
2 acid sequence at least 94% identical to SEQ ID NO:2, wherein the polypeptide exhibits
3 polymerase activity.
- 1 16. The isolated nucleic acid of claim 15, wherein the polypeptide
2 comprises SEQ ID NO:2.
- 1 17. The isolated nucleic acid of claim 15, wherein the nucleic acid
2 comprises SEQ ID NO:1.
- 1 18. The isolated nucleic acid of claim 15, wherein the polypeptide further
2 comprises a DNA binding domain.

- 1 19. The isolated nucleic acid of claim 18, wherein the DNA binding
2 domain is selected from the group consisting of Sso7d, Sac7d, and Sac7e.
- 1 20. The isolated nucleic acid of claim 19, wherein the DNA binding
2 domain is Sso7d.
- 1 21. The isolated nucleic acid of claim 19, wherein the nucleic acid
2 comprises SEQ ID NO:3.
- 1 22. The isolated nucleic acid of claim 19, wherein the nucleic acid encodes
2 a polypeptide comprising SEQ ID NO:4.
- 1 23. An expression vector comprising the nucleic acid of claim 15.
- 1 24. A host cell transfected with the vector of claim 23.
- 1 25. An isolated polypeptide, wherein the polypeptide comprises an amino
2 acid sequence at least 94% identical to SEQ ID NO:2, and wherein the polypeptide has
3 polymerase activity.
- 1 26. The isolated polypeptide of claim 25, wherein the polypeptide
2 comprises SEQ ID NO:2.
- 1 27. The isolated polypeptide of claim 25, further comprising a DNA
2 binding domain.
- 1 28. The isolated polypeptide of claim 27, wherein the DNA binding
2 domain is selected from the group consisting of Sso7d, Sac7d, or Sac7e.
- 1 29. The isolated polypeptide of claim 27, wherein the DNA binding
2 domain is fused to the carboxy-terminus of the polypeptide.
- 1 30. The isolated polypeptide of claim 29, wherein the DNA binding
2 domain is Sso7d.
- 1 31. The isolated polypeptide of claim 30, wherein the polypeptide
2 comprises SEQ ID NO:4.

1 32. A method of amplifying a target sequence using a hybrid polymerase,
2 the method comprising the steps of:
3 providing a polymerase according to claim 1 or claim 25,
4 combining the polymerase in an amplification reaction mixture, and
5 amplifying the target sequence.